

WO 01/53312

PCT/US00/34263

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=-Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
			ASYNVNPLSSTAQSTSARNNSDSKLTWSPGSVTNTSLAHELWKVP LPKKNITAPSRRPPGTLGKPPPLSTWDNSPLRIGGGWGNSDARY TPGSWGESSGRITNWVLKNCNLPQIDGSTLRTLICMQHGPLIT FHLNLPHGNALVRYSKEEVVKAQKSLHJSDLFLTL
7117	695	1261	LLISTPGGCHPPPSSIEFTYIGAWGKALPAHMPCAPGALPQGA FVSQAARAIPLLQPSQAAQAEGLSQPARACGALCSPWPLRNWG SPILRLPGLLRTPTNDRKTRTRSACWARAQWDTLGPLKLSHR GKVCRLHRPRTGVRGGPGAAQRQGGMGTRRGTFTSGARDPGGL RVKHRCOPTGHLF
7118	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLAKEVEEISLLQPQE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGCDPKIGAAIQEELGYNCCTGGVIAEI LRGVRLHFHNLVKGTLDSLACKAQLGLGHGSYSRAVKFVNVRDV NMIIQSISLLDQLDKDINTFSMRVREWYCYHFPVELVKIINDNAT YCRLAQFIGNRRELNEDEKLEELTMGDAKAKAILDARSSMG MDISAIIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSL ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEMVQAE EAAAETRKLEKQEKKRLLKEKKRLLAALALASSENSSSTPEECE EMSEKPKKKKKQKQPQEVPOENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKETVNDPEEAGRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLAKEVEEISLLQPQE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGCDPKIGAAIQEELGYNCCTGGVIAEI LRGVRLHFHNLVKGTLDSLACKAQLGLGHGSYSRAVKFVNVRDV NMIIQSISLLDQLDKDINTFSMRVREWYCYHFPVELVKIINDNAT YCRLAQFIGNRRELNEDEKLEELTMGDAKAKAILDARSSMG MDISAIIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSL ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEMVQAE EAAAETRKLEKQEKKRLLKEKKRLLAALALASSENSSSTPEECE EMSEKPKKKKKQKQPQEVPOENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKETVNDPEEACHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED
7120	1991	64	QIGTRRCLRGDKVTNAQDFLVTNLRFRTFEPQTANLSVVFKDS NSTTPLIFVLSPTGTDPAADLYKFAEEMFKSKLSSAISLQGQGP RAEAMMRSSIERGKWWFFQNCHLAPSWMALERLIEHINPDKVH RDRFLWLTSPLPSNKFVPSILONGSKMTIEPPRGVRANLILKSYSS LGEDFLNSCHKVMFKSLLLSSLCLFHGNALERRKFGPILGFNPY EFTDGDLRICISQLKMFLDEDDYPIVKVLYKTAGEINYGGRTD DWDRRCIMNILEDFYNEDVLSPEHSYSASGIYHQIPTYDLHGY LSYIKSLPLNDMPEIFGLHDNNANITFAQNETFALLGTTIOLOKP SSSAGSQGREEIVEDVTQNIILLKVPPEPINLQWVMAKYPVLYEES MNTVLVQEVRIRNLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNNTVPELWSAKAYPSLKPSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFQFLGTLQNFARKFVISIDTISDFKVMFE APSELTQRPVQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWLPTPNRAKAQDQDFYLCPITYKTLTRAGTLSTTGHSTNYVI AVEIPTHPQPRHWIKRGVVALCALDY
7121	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLSDDTMRRRLIPPFREASAK LTTLVADAEAAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTAAETVASLWPALQELARCNGNLACRSDLQVAAKALEMGVF GAYFNVLINLRDITDEAFKDQIHRVSSLQEAKTQAAVLVDCL

WO 01/53312

PCT/US00/34263

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ETRQE
7122	2	546	RPLRPWVLSQLGSMVGMLMTYGRQRQFQSLSDTMRRRLIPPFREASAKLTTLVDAAEATAYLEAMRLPKNTPEEKDRRTAACLOEGLRRAVSPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF GAYFNVLINLRDITDEAFKDQIHHRVSSLQEAKTQAAVLVDCL ETRQE
7123	1	1092	KPAVPEARSAGTSEAGRSGAAEVSCGSVSGDGAAMRLTPRALCS AAQAAWRRENFPILCGRDVARWFPGHMAKGLKKMQSSLKLVDCIIE VHDARIPLSGRNPLFQETLGLKPHLLVLNKMDLADLTREQQKIMQ HLEGEGLKNVIFTNCVKDENVKQIIIPMVTIELIGRSHYHRKENL EYCIMIVGPVNKGKSSLINSLRRQHLRKSKATRVGGEPGITRAV MSKIQVSEERPLMFLLDTPGVLAAPRIESVETGLKLALCGTVLDHL VGEETMADYLTYTLNKHQRFGYVQHYGLGSACDNVERVLKSVAV KLGKTQKVVLGTGTVNVNVIQPNPYAAARDFLQTFRRLGLGSVM LDLDVLRGHPRV
7124	2	382	LPPLTLLAAPFAHLLPPPGHDQSPCWHPGPALSPGTLGPLSWAM ANSGLQLLGFLALGGWVGIIASTALPQWKQSSYAGDASIQLRS KVFVLESEWGDSLGLPRDCGWSCLLHSAVRSEKGFW
7125	166	1127	NCISEKRNYSFMSMQKGKGRTSRIRRKLCGSSSERGVNESHKSE FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLOEGQMIIS LPESCLLT\RDTCVIRSYLGYAITKWKPPSPLLA\CTFLVSEKH AGHRSLEA\YLEILPKAYTCPVCLEPEVVNLLPKSLKAKAEEQ RAHVQEFFFASSRDFSSLQPLFAEAVDSIFSYSALLWAWCTVNT RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHSPHVQVKAFA ETHSYEIRTTSRWRKHEEVFICYGPHDNRQRLFLEYGFVSVHNPH ACVYVSRGWNQLCS
7126	1	733	CRDMAAFIVPSARRCSQKGSLGHLPTQPWLAAMSPrGQERGT SHSQAREPQRPGRNLLGSLQSSPGTLGQAGTASRRRQCMVQRWV QVATGRRAVQVPKGALGLALGETSPGASRGMSGGAGGCWALGWA PSPVLPWLPGPPWPLSIISDSDGTQRPSPRRCPARPSPWGPQC WRGGRIASAEASST*TPGSGSRARSGRRSPGSRRRSASAPSPTP PTDACA*SCVARPAGSRSSRPAAA
7127	1311	277	GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKET*RRIPIRF AKQKQI*S*NSQKIGASEIDRGRKEADCSDAPAAARIHAVSVF RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLLFHTPEQFLAEC ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VLFRI*WLKDCDV *FCQKIFATNCWNQNLIQ*EE*KPVEYSVEN*HIMNLLPML CQSSLRDQTIIVTWRM*RNYSMFRNMISL*DGSIHIPLKLHFY PALIFTLTVPINSCQRPLPLFAHQSIKTLASSGSPMLACRFL LVKKRAFIHTPRSPGCSV*CKHVLVKDNKNNCVGSEV
7128	2	5228	GRVDLWTILEGSRALRELQTEAEELNKHWRRLLLEGLSYYKPPSP SSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCYLQE DYRGTRDSVKTWLQDERQSQUALILKIAADYYEEERTCILRCVHL LTYFQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTEAPT WEFHGNLMTERQVSRFVQCLREQSMLEIIIFLYYAYFEMAPSD LLVLTKMFKEQGFSRQTNRHLVDETMDPFDVDRIGYFSALILVE GMDIESLHKCALDDRRELHQFAQDGGLICQDMDCMLTFGDIPHH APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYLTLLQ SLASGGNDCTTSTAACMCVYGLSFVLTSLLEHTLGNQQDIIDTA CEVLADPSSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLL RALVSGKSTAKVYFLDKMSFYNELYKHKPHDVISHEGTLWR RQTPKLLYPLGGQTNLRIIPQGTVGQVMLDDRAYLVRWEYSYSSW TLETCIEIEMLLHVVSTADVIQHCORVKPIIDLVHKVISTDLSIA DCLLPITSRIYMLLQLRLTTVISPPVDVIASCVNCLTVLAARNPA KWWFDLRLRHTGFLPFVAHPVSSLQISMIAEGMNAGGYGNLLMNSE OPOGEYGVTAFLRLITTLVKGQLGSTSQGLVPCVMFVLKEMI

WO 01/53312

PCT/US00/34263

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
			PSYHKWRYNNSHGVRQIGCLILEHILNLCHETDLHSSTPS LQFLCICSLAYTEAGQTVINIMGIVGDTIDMVMAAQPRSDGAEG QGGQQLIKTVKLAFTSVNTNVRILKPPSNVVSPLQALSQHGAH GNNLJIAVLAKYIYHKHDPALPRLAQLIJKRLATVAPMSVYACLG NDAAAIRDAFLTRLQSK\IE\DMRIKVML\EFLTVA\VEQP GLIELFLNLEVKGDG\SDGSKEFSLGMW\SCLHAV\WVELIDSQQ QDRYWCPLLHRAAIAFLHALWQDRRDSAMLVLRLTPKFWENLT SPLFGTILSPSETSEPSILETCALIMKIICLEIYYVVKGSLDQP LKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLLEYQM LVAWRMILLIATTHADIMHTDSVRRQLFLDVLDGKTKALLLV PASVNCLRLGSMKCTLILLRLROWKRELSGVDEILGPLTEILEG VHQADQQLMEKTKAKVFSAFITVILQMKEMKVSDIPQYSQVLNV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQ RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLTTLEV SLRMKQNLHFTEAHLHLLARTQQGATAVAGAGITQSICLPL LSVYQLSTNGTAQTPSASRKSLDAPSWPVGVYRLSMSLMEQLLKT LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEDHTVG FILQLSNFMKEWHFHPQLMRDIQVNLGYLCQACTSFLHSRKML QHYLQNKNQGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAADTE ASEQQALHTVQYGLLKILSCTLAAALRHFTPDVCQILLDQSLDIA EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELEDKKK EPLTQAVGLSTQAEGTRTLKSLLMFTMENCYLLISQAMRYLIRD PAVHPRDQRMKQELSELSTLSSLSRYFRRGAPSPATGVLP SPOGKSTSLSKASPESQEPLIQQLVQAFVRHMQR
7129	1	1054	FRRFRWRRRLH*AGPASSACCGSPGEASGTMGELPPNNIKEPR WDQSTFIGRANHFFTVDPRNILLTNEQLESARKIVHDYRQGIV PPGLTENELWRAKYIYDSAFHPDTGEKMLIGRMSAQVMNMTI TGCMMTFYRTTPAVLFQWQWINQSFNAVVNYTNRSGDAPLTNVEL GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAACNI NIPLMRQRELKVGIPVTDEGNRLGESANAAKQAITQVUVSRIL MAAPGMAIPPFIMNTLEKKAFRFPWMSAPIQVGLVGFCLVFA TPILCALFPQKSSMSVTSLEALQAKIQESHPELRRVYFNKL
7130	2	780	HEVPSLQTSMDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLRKG ISAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQQLSLHRSSS RCESHQDLLPDIADSHHQGTEKLSDLTLQDSQKVVVNRNLPLN AQIATQNYFSNFKETDGDEDDEYVEIKSEEDESELELSHNRRRKS DSKFVDADFSDNVCSGNTLHSLSNPRTPKKPVNSKGLSPYLTP YNDSDKLNDYLWRGPSPNQONIQVQLREKFQCLSSSSFA
7131	805	573	AAAEGHIEVVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLEVV KLLQDYQDSYTLSETQAEAAAELSKENLESMV
7132	1420	1087	IDMLLLSGALVSGPYTLITTAVASDLGTHKSLKGNAHALSTVTA IIDGTGSVGAALGPPLLALGSPSGWSNVFYMLMFADACALLFLI RLIHKELSCPGSATGDQVPFKEQ
7133	2	3648	QQIPGLLPAHGESGDALKRPLQKPKITGHLDLFFTLYPSLEKF EEELLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGFVQ RPQVVLVLPEDMVALTRSASFSLRKVVSSSKTSSGSQALVLSRSL RLPEMVGHPAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLACMH MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSPHCLVYKVPASAMS SEEVKQVESGTLRFQFSLGSSEEHLDAPTEPVSGPKVERRPSRKP PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPQTQHCL ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS IAEQLQELPFTPLHAPIVVGQTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTNPQKEESDCLOSNEMLQFLAFLS RVAQDCRGTSWPKTVYFTQFYRFPATTPRLQLVQLDEAGQPS SGALTHILVPVSRDGTFDAGSPGFQLRYMVGPGFLKPGERRCFA RYLAVQTLQIDVWDGDSLLLIGSAAVQMKHLLRQGRPAVQASHE

WO 01/53312

PCT/US00/34263

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
			LEVVATEYEQDNMVVSGDMLGFRVKPIGVHSVVKGRLHLLAN VGHPCEQKVRGCSTLPPRSRVSVISNDGASRFSGGSLLTTGSSRR KHVVQAQKLAQDSELAAMLLTHARQGKGPQDVRESDATRRRK LERMRSVRLQEAGGDLGRGRTSVLAQQSVRTQHLRDLQVIAAYR ERTKAESTASLSLAITTEHTLHATLGVAEFFEFVLKNPHNTQH TVTVEIDNPELSVIVDSQEWRFKGAAGLHTPVEEDMFHLRGSL APQLYLRPHEATAHVPFKPQSFSAGQLAMVQASPGLSNEKMDAV SPWKSSAVPTKHAKVLFRASGGKPITAVLCLTVELQPHVVDQVFR FYHPELSFLKKAIRLPPWHTFPGAPVGMIGEDPPVHVRCSDPNV ICETQNVPGEPRDIFLKVASGSPPEIKDFFVIYSDRWLATPT QTWQVYLHSLQRVDVSCVAGQLTRLSLVLRGTQTVRKRAFTSH PQELKTDPKGVFVLPPLPRGVQDLHVGVPRIRAGSRFVHNLDV CHQLVASWLVCCLCRQPLISKAFEMIILAAGEGKGVNKRITYTNP YPSRRTFHLHSDHPELLRFREDSFQVGGGETYTIGLQFAPSQRV GEEILLYINDHEDKNEEAFCVKVIYQ
7134	2115	1111	GGEFGSYPPHVGLSLGTPLDPHYVLLLEVHYDNPTYEEGLIDNSG LRLFYTMDDIRKYDAGVIREAGLWVSLFHTIPPGMPEFQSEGHTL ECLEEALEAEKPSGIHVFALLNHAIAGR GIRLRLHFRKGKEMKL LAYDDDFDNFQEFQYLKEEQTILPGDNLITECRYNTKDRAEMT WGGLSTRSEMCLSYLLYYPRINLTCASIPDIMEQLQFIGVKET YRPVTWTWPFIIKSPKQYKNL SFMDAMNKPKWTKKEGLSFNKLVL SPLVNVRCSKTDNAEWSIQGMTALPPDIERPYKAEPLVCGTSSS SSLHRDFTSINLLVCLLSCTLSTKSL
7135	2	2072	FVPRVTFRSLSLQGPKGESVGSITQPLPSSYLIFRAASESDGRC WLDALLELALRCSSLLRLGTCPKGRDGEPGTSPDASPSSLGGLPA SATVHPDQDLFPNLNGSSLENDAFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQEEELGELGEASQVETVSE ENKSLMWTLKQLRPGMDLSRVVLLPTFVLEPRSFLNKLSDYYH ADLLSRAAVEEDAYSRMKLVRLWYLSGFYKKPKGLIKKEYNPILG ETFRCCWFHPQTSRIFTYIAEQVSHHPPVSAFHVSNRKGFCIS GSITAKSRFYGNLSALLDGKATLTFLNRAEDYTLTMFYAHCKG ILYGTMTLELGKVIECAKNNFQAOLEFKLKPFFGSTSINQI SGKITSGEEVLASLSGHWDRDVFIKEEGGSSALFWTFSGEVRR QRJRHVTPLLEQTELESERLWQHVTRAISKGDQHRAIQEKFAL EEAQQRARERQESLMWPQKQLFHLDPITQEWHYRVEDHSPWDP LKDIAQFEQDGILRTLQQEAVARQTFLGSPGPRHERGSPDQRL RKASDQPSGHQSATESSGSTPESCPELSDEEQDGFVPGGESCP PRCRKEARRLQALHEAILSIREAQOBELHRLSAMLSSTARAAQA PTPGLLQSPRSWFLLCFLACQLFINHILK
7136	2	418	DFVPSFRPESGNTSQTWLLRAATLEKEVAGLREKIHLLDDMLK SOORKVROMIEQLQNSKAVIQSKDATIQELKEKTIAYLEAENLEM HDMHELIKEKQISHGNFSTQARAKTENPGSIRISKPPSPKMPMV IRVVEH
7137	2	466	WASGMSTVPGGSRHSLGIVQRGGWGVGTGEEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRQKKGVPFLGDFLTELQR LDSAI PDDLDGNTNKRSKEVRLVQEMQLLQVAAMNYRIRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP
7138	2	466	WASGMSTVPGGSRHSLGIVQRGGWGVGTGEEEESLTVPVADTWQA GSFKVATQERNPQRAQMRLRQKKGVPFLGDFLTELQR LDSAI PDDLDGNTNKRSKEVRLVQEMQLLQVAAMNYRIRPLEKFVTYFT RMEQLSDKESYKLSCQLEPENP
7139	1	357	SRLNSARGLKMASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRLGWVQFSSEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDDEKKDF
7140	1401	1957	RASSLQLVKAWGCLIPSSFQQQHTGOYALEELFDLKVDCCFSF NMNVSLEKQLRPSQPWPRGKCRKTPGWEEARPKAQDLRGDLGKT

WO 01/53312

PCT/US00/34263

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * =Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
			QAGPAEAHTRGPPRPLPAATGCPPHLPGLLSGISVDIDPTGLQSQWTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNFADFMNTNQCG
7141	124	1073	LDSRSCWLDMEDLEEDVRFIVDETLDFFGLSPSDSREEDITVLVTEPKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFLVKDSP VRDLLPTVNSLTRLSTPS/LKQPDASTPE***EGVSQGSPGYIWKEALQHEEGVTHLQSVPICIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAKSSSQLPIPSAIPRPASRMLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRNLNPVM GATRSNLQPP
7142	658	839	LIFLMLHMEALKMILSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVCRT/YSSDLQVGVIKPWLLLGSODAAHLDLT LKKNKVTHILNVAYGVENAFLSDFTYKSIISILDI,PETNILSYFP ECFEFIEEAKRKDGVVVLVHCNA
7143	3	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDTIISGRSTPAMMNGQ GSTTSSSKNIAYNCNWDCQOACFNSSPDLDHIRS1HVDGQRGG VFVCLWKGCKVNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSSVFHFSTVSILLFFQIKYKTLQKNISTIISKSLKI
7144	1	988	FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPPAGVSVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHHTDWNDIVLCCNGKTLISASS DTTVKVWNNAHKGFCMSTLRTKDYVKALAYAKDKELVASAGLDR QIFLWDVNTLTALTASNTVTSSLGKDSIYSLAMNQLGTII VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLNRDGTQCLS GSSEDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG RDRKIYCTDLRNPDIRVLICE

TRADOCS:1416260.1(%CSK01!.DOC)

WO 01/53312

PCT/US00/34263

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

WO 01/53312

PCT/US00/34263

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
 - a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
 - a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

WO 01/53312

PCT/US00/34263

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

WO 01/53312

PCT/US00/34263

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.
21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

<http://www.patentlens.net>

Image is corrupt.

INTERNATIONAL SEARCH REPORT		International application No. PCT/US00/34263																					
A. CLASSIFICATION OF SUBJECT MATTER IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00 US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350 According to International Patent Classification (IPC) or to both national classification and IPC																							
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 536/23.1; 435/320.1, 455, 468, 530/300, 350																							
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched																							
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) MEDLINE, EAST																							
C. DOCUMENTS CONSIDERED TO BE RELEVANT <table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="text-align: left;">Category *</th> <th style="text-align: left;">Citation of document, with indication, where appropriate, of the relevant passages</th> <th style="text-align: left;">Relevant to claim No.</th> </tr> </thead> <tbody> <tr> <td>A</td> <td>WAJIMA et al. The cDNA cloning and transient expression of an ovary-specific 17beta-hydroxysteroid dehydrogenase of chickens. Gene. 1999, Vol.233, pages 75-82</td> <td>1-11, 13-16, and 19-26</td> </tr> <tr> <td>A</td> <td>US 5,175,095 A (MARTINEAU et al) 29 December 1992 (29.12.1992), see especially columns 3-18.</td> <td>1-11, 13-16, and 19-26</td> </tr> <tr> <td>A</td> <td>Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract.</td> <td>1-11, 13-16, and 19-26</td> </tr> <tr> <td>A,P</td> <td>Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract.</td> <td>1-11, 13-16, and 19-26</td> </tr> <tr> <td>A</td> <td>Database PubMed, ID No. 2760883, BEIL et al. Synthesis of polypeptides by the cervix of the baboon (Papio anubis). J. Reprod. Fertil. July 1989. Vol.86. No.2. pages 535-544, see Abstract.</td> <td>1-11, 13-16, and 19-26</td> </tr> <tr> <td>A,P</td> <td>Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract.</td> <td>1-11, 13-16, and 19-26</td> </tr> </tbody> </table>			Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.	A	WAJIMA et al. The cDNA cloning and transient expression of an ovary-specific 17beta-hydroxysteroid dehydrogenase of chickens. Gene. 1999, Vol.233, pages 75-82	1-11, 13-16, and 19-26	A	US 5,175,095 A (MARTINEAU et al) 29 December 1992 (29.12.1992), see especially columns 3-18.	1-11, 13-16, and 19-26	A	Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract.	1-11, 13-16, and 19-26	A,P	Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract.	1-11, 13-16, and 19-26	A	Database PubMed, ID No. 2760883, BEIL et al. Synthesis of polypeptides by the cervix of the baboon (Papio anubis). J. Reprod. Fertil. July 1989. Vol.86. No.2. pages 535-544, see Abstract.	1-11, 13-16, and 19-26	A,P	Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract.	1-11, 13-16, and 19-26
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.																					
A	WAJIMA et al. The cDNA cloning and transient expression of an ovary-specific 17beta-hydroxysteroid dehydrogenase of chickens. Gene. 1999, Vol.233, pages 75-82	1-11, 13-16, and 19-26																					
A	US 5,175,095 A (MARTINEAU et al) 29 December 1992 (29.12.1992), see especially columns 3-18.	1-11, 13-16, and 19-26																					
A	Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract.	1-11, 13-16, and 19-26																					
A,P	Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract.	1-11, 13-16, and 19-26																					
A	Database PubMed, ID No. 2760883, BEIL et al. Synthesis of polypeptides by the cervix of the baboon (Papio anubis). J. Reprod. Fertil. July 1989. Vol.86. No.2. pages 535-544, see Abstract.	1-11, 13-16, and 19-26																					
A,P	Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract.	1-11, 13-16, and 19-26																					
<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.																							
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed																							
Date of the actual completion of the international search		Date of mailing of the international search report <i>07 JUN 2001</i>																					
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230		Authorized officer <i>Michael Woodward</i> Michael Woodward Telephone No. (703)308-0196																					

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
This includes 4 invention Groups and 3572 sequence species

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group III, claims 17-18, drawn to methods of identifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containing same, respectively, and methods of making as well as the first method of use of this subject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different method than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.